



## SEQUENCE LISTING

<110> Kelly, Kathleen  
The Government of the United States of America  
as represented by The Secretary of the  
Department of Health and Human Services

<120> Methods and Compositions for Inhibiting Inflammation  
and Angiogenesis Comprising a Mammalian CD97 Alpha  
Subunit

<130> 015280-263100US

<140> US 09/284,819

<141> 1999-08-20

<150> US 60/027,871

<151> 1996-10-25

<150> WO PCT/US97/19772

<151> 1997-10-24

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-1 EGF-like  
repeat conserved motif

<400> 1

Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser Cys Val  
1 5 10 15

Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe Ser Glu  
20 25 30

Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp  
35 40

<210> 2

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-2 EGF-like  
repeat conserved motif

<400> 2

Asp Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe  
1 5 10 15

Ser Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro  
20 25 30

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Gly Tyr Glu Pro Val Ser Gly Thr Lys Thr Phe Lys Asn Glu Ser Glu  
35 40 45

Asn Thr Cys Gln  
50

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<210> 3
<211> 44
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence:EGF-3 EGF-like repeat conserved motif

```

<400> 3
Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly
  1             5             10             15
Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly
      20             25             30
Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr
    35             40

```

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<210> 4
<211> 49
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence:EGF-4 EGF-like repeat conserved motif

```

<400> 4
Asp Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr
  1             5             10             15
His Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly
          20             25             30
Trp Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys
      35             40             45

```

Glu

```
<210> 5
<211> 49
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:EGF-5 EGF-like
repeat conserved motif
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<400> 5  
Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr  
1 5 10 15

Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly  
                   20                  25                  30

Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys  
           35                  40                  45

Glu

<210> 6  
 <211> 835  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CD97amino acid sequence encoded by full-length  
           clone pAT276

<400> 6  
 Met Gly Gly Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro  
   1                  5                  10                  15

Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln  
                   20                  25                  30

Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe  
           35                  40                  45

Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp  
           50                  55                  60

Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser  
   65                  70                  75                  80

Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly  
                   85                  90                  95

Tyr Glu Pro Val Ser Gly Thr Lys Thr Phe Lys Asn Glu Ser Glu Asn  
           100                  105                  110

Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys  
           115                  120                  125

Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys  
   130                  135                  140

Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp  
  145                  150                  155                  160

Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr His  
                   165                  170                  175

Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly Trp  
           180                  185                  190

Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys Glu  
           195                  200                  205

Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr  
   210                  215                  220

Val	Cys	Phe	Asn	Thr	Val	Gly	Ser	Tyr	Ser	Cys	Arg	Cys	Arg	Pro	Gly	225	230	235	240
Trp	Lys	Pro	Arg	His	Gly	Ile	Pro	Asn	Asn	Gln	Lys	Asp	Thr	Val	Cys	245	250	255	
Glu	Asp	Met	Thr	Phe	Ser	Thr	Trp	Thr	Pro	Pro	Pro	Gly	Val	His	Ser	260	265	270	
Gln	Thr	Leu	Ser	Arg	Phe	Phe	Asp	Lys	Val	Gln	Asp	Leu	Gly	Arg	Asp	275	280	285	
Ser	Lys	Thr	Ser	Ser	Ala	Glu	Val	Thr	Ile	Gln	Asn	Val	Ile	Lys	Leu	290	295	300	
Val	Asp	Glu	Leu	Met	Glu	Ala	Pro	Gly	Asp	Val	Glu	Ala	Leu	Ala	Pro	305	310	315	320
Pro	Val	Arg	His	Leu	Ile	Ala	Thr	Gln	Leu	Leu	Ser	Asn	Leu	Glu	Asp	325	330	335	
Ile	Met	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Pro	Lys	Gly	Pro	Phe	Thr	Tyr	340	345	350	
Ile	Ser	Pro	Ser	Asn	Thr	Glu	Leu	Thr	Leu	Met	Ile	Gln	Glu	Arg	Gly	355	360	365	
Asp	Lys	Asn	Val	Thr	Met	Gly	Gln	Ser	Ser	Ala	Arg	Met	Lys	Leu	Asn	370	375	380	
Trp	Ala	Val	Ala	Ala	Gly	Ala	Glu	Asp	Pro	Gly	Pro	Ala	Val	Ala	Gly	385	390	395	400
Ile	Leu	Ser	Ile	Gln	Asn	Met	Thr	Thr	Leu	Leu	Ala	Asn	Ala	Ser	Leu	405	410	415	
Asn	Leu	His	Ser	Lys	Lys	Gln	Ala	Glu	Leu	Glu	Glu	Ile	Tyr	Glu	Ser	420	425	430	
Ser	Ile	Arg	Gly	Val	Gln	Leu	Arg	Arg	Leu	Ser	Ala	Val	Asn	Ser	Ile	435	440	445	
Phe	Leu	Ser	His	Asn	Asn	Thr	Lys	Glu	Leu	Asn	Ser	Pro	Ile	Leu	Phe	450	455	460	
Ala	Phe	Ser	His	Leu	Glu	Ser	Ser	Asp	Gly	Glu	Ala	Gly	Arg	Asp	Pro	465	470	475	480
Pro	Ala	Lys	Asp	Val	Met	Pro	Gly	Pro	Arg	Gln	Glu	Leu	Leu	Cys	Ala	485	490	495	
Phe	Trp	Lys	Ser	Asp	Ser	Asp	Arg	Gly	Gly	His	Trp	Ala	Thr	Glu	Gly	500	505	510	
Cys	Gln	Val	Leu	Gly	Ser	Lys	Asn	Gly	Ser	Thr	Thr	Cys	Gln	Cys	Ser	515	520	525	
His	Leu	Ser	Ser	Phe	Ala	Ile	Leu	Met	Ala	His	Tyr	Asp	Val	Glu	Asp	530	535	540	

Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe  
 545 550 555 560  
 Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln  
 565 570 575  
 Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val  
 580 585 590  
 Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val  
 595 600 605  
 Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu  
 610 615 620  
 Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu  
 625 630 635 640  
 Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys  
 645 650 655  
 Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala  
 660 665 670  
 Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe  
 675 680 685  
 Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile  
 690 695 700  
 Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln  
 705 710 715 720  
 Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg  
 725 730 735  
 Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr  
 740 745 750  
 Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr  
 755 760 765  
 Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu  
 770 775 780  
 Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp  
 785 790 795 800  
 Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr  
 805 810 815  
 Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu  
 820 825 830  
 Ser Gly Ile  
 835

<210> 7  
 <211> 3  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:RGD motif  
 binding site for several classes of integrins

<400> 7  
 Arg Gly Asp  
 1

<210> 8  
 <211> 3156  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> full length pAT276 encoding CD97

<220>  
 <221> CDS  
 <222> (49)..(2556)  
 <223> CD97

<400> 8  
 ctgtcccact cactctttcc cctgccgctc ctgccggcag ctccaacccat gggaggccgc 60  
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 ggtgtgtccc ggtggtgccc tcagaactcc tcgtgtgtca atgccaccgc ctgtcgctgc 180  
 aatccagggt tcagctcttt ttctgagatc atcaccaccc cgacgggagac ttgtgacgac 240  
 atcaacgagt gtgcaacacc gtcgaaagtg tcatgcggaa aattctcgga ctgctggaac 300  
 acagagggga gctacgactg cgtgtgcagc ccgggatatg agcctgtttc tgggacaaaa 360  
 acattcaaga atgagagcga gaacacctgt caagatgtgg acgaatgtca gcagaaccca 420  
 aggctctgta aaagctacgg cacctgcgtc aacacccttg gcagctatac ctgccagtgc 480  
 ctgcctggct tcaagttcat acctgaggat ccgaaggctc gcacagatgt gaatgaatgc 540  
 acctccggac aaaatccgtg ccacagctcc acctactgcc tcaacaacgt gggcagctat 600  
 cagtgtcgct gccgaccggg ctggcaaccg attccggggg cccccaatgg cccaaacaat 660  
 accgtctgtg aagatgtgga cgagtgcagc tccgggcagc atcagtgtga cagctccacc 720  
 gtctgcttca acaccgtggg ttcatacagc tgccgctgcc gcccgaggctg gaagcccaga 780  
 cacggaatcc cgaataacca aaaggacact gtctgtgaag atatgacttt ctccacctgg 840  
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 gtcaactcca tctttctgag ccacaacaac accaaggaac tcaactcccc catccttttc 1440  
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 ggcggccagg tggggctgct ctgccgcctg gtggccgggc tgctgcacta ctgtttcctg 1920  
 gccgccttct gctggatgag cctcgaaggc ctggagctct actttcttgt ggtgcgcgtg 1980

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ttccaaggcc agggcctgag tacgcgctgg ctctgcctga tcggctatgg cgtgcccctg 2040
ctcatcgtag gcgtctcggc tgccatctac agcaagggtt acggccgccc cagatactgc 2100
tggttggaact ttgagcaggg cttcctcttg agcttcttgg gacctgtgac cttcatcatt 2160
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ttggggccac tgcctgaggc tcacggtaca gaggcctgcc ctgcctggcc gggcaggagg 3060
ttctcactgt tgtgaagggt gtagacgttg tgtaatgtgt ttttatctgt taaaattttt 3120
cagtgttgac acttaaaatt aaacacatgc atacag 3156

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<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:5' PCR primer
276-38

```

```

<400> 9
ggccgcgtct ttctcgca 18

```

```

<210> 10
<211> 17
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:5' PCR primer
276-20

```

```

<400> 10
agatgtggac gaatgtc 17

```

```

<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence:5' PCR primer
276-6A

```

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<400> 11
aagacaagct cagccga 17

```

<210> 12  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' PCR primer  
 276-3

<400> 12  
 tgggttcata cagctgc

17

<210> 13  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' PCR primer  
 276-6B

<400> 13  
 tcggctgagc ttgtctt

17

<210> 14  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' PCR primer  
 276-15B

<400> 14  
 gcagctgtat gaaccca

17

<210> 15  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:anti-EGF3  
 peptide used for antibody production

<400> 15  
 Cys Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys  
   1                  5                  10                  15

<210> 16  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:anti-COOH  
 peptide used for antibody production



<400> 16

Glu Phe Thr Ser Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala  
 1 5 10 15

<210> 17

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide  
 amplification primer

<400> 17

atgggaggcc gcgtctttct cgcattctgt gt

32

<210> 18

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide  
 amplification primer

<400> 18

gggccctcag ggcacagag tccggcata

29

<210> 19

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-like repeat  
 conserved motif in fibrillin

<220>

<221> MOD\_RES

<222> (1)..(41)

<223> Xaa = any amino acid

<400> 19

Asp Ile Asp Glu Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Gly Xaa  
 1 5 10 15

Cys Xaa Asn Thr Xaa Gly Ser Tyr Xaa Cys Xaa Cys Xaa Xaa Gly Phe  
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 35 40

<210> 20

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-like repeat  
conserved motif in EMR1

<220>

<221> MOD\_RES

<222> (1)..(48)

<223> Xaa = any amino acid

<400> 20

Asp Ile Asp Glu Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Cys Xaa Asn Xaa Xaa Gly Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa Gly  
20 25 30

Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
35 40 45

<210> 21

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Asp/Asn  
beta-hydroxylation consensus motif

<220>

<221> MOD\_RES

<222> (1)..(12)

<223> Xaa = any amino acid

<400> 21

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys  
1 5 10